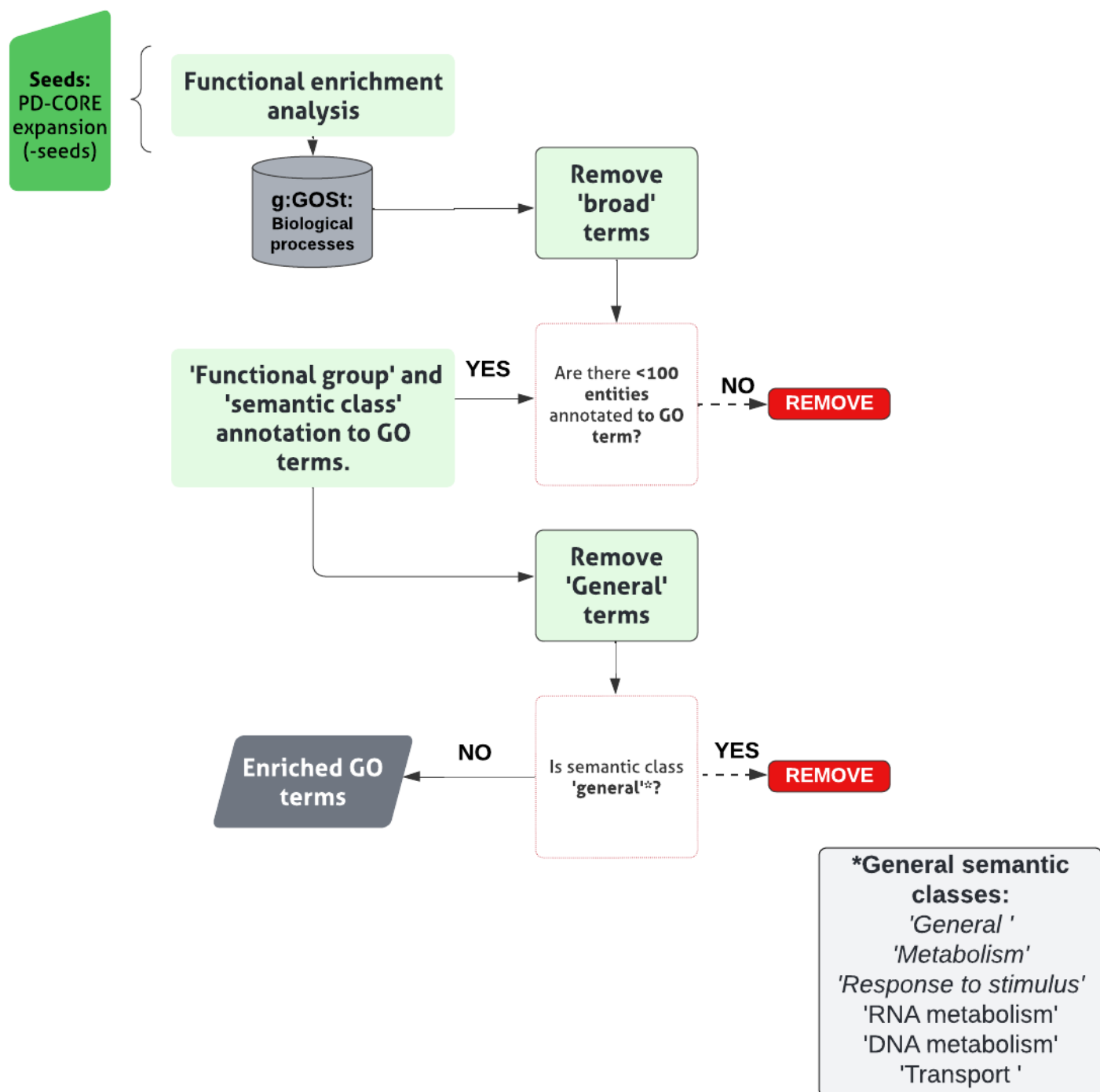
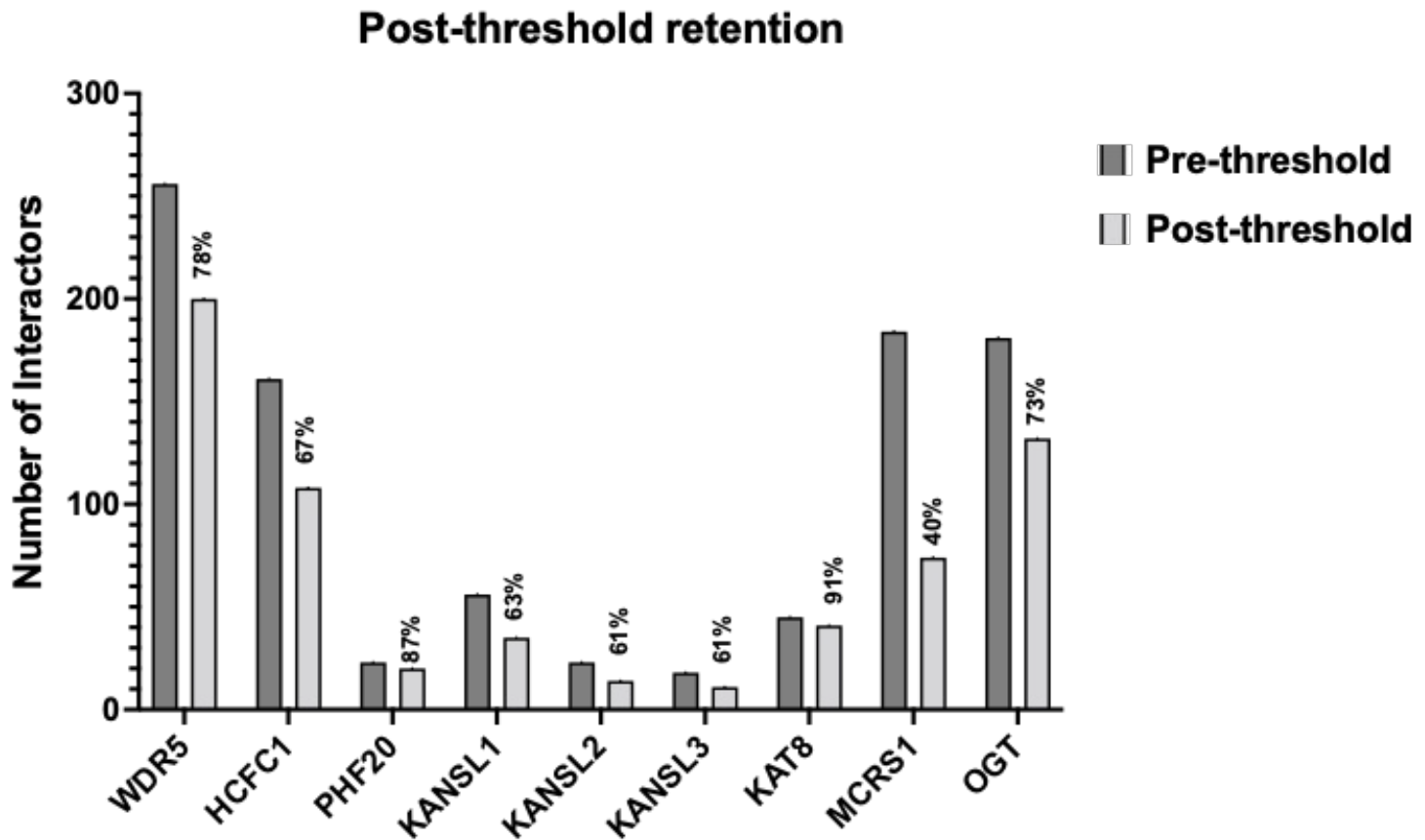


Supplementary figure 1



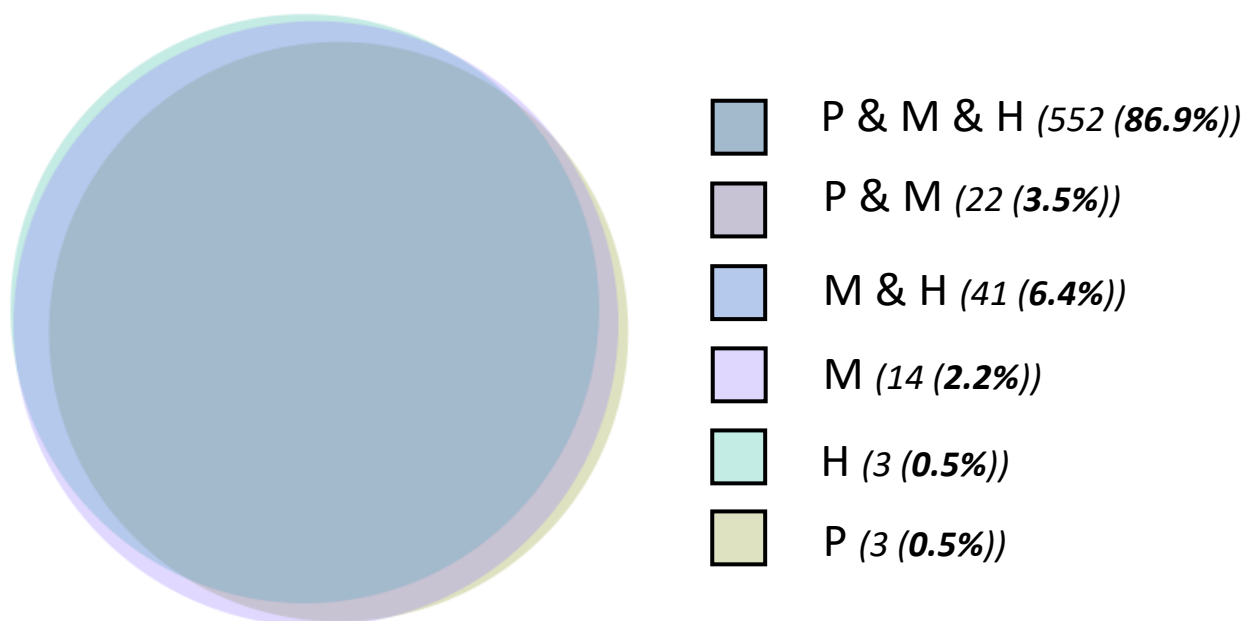
Supplementary figure 1. Functional Enrichment general pipeline. The grey box indicates Semantic Classes (SCs) removed from the analysis, as they are classified as 'general'.

Supplementary figure 2



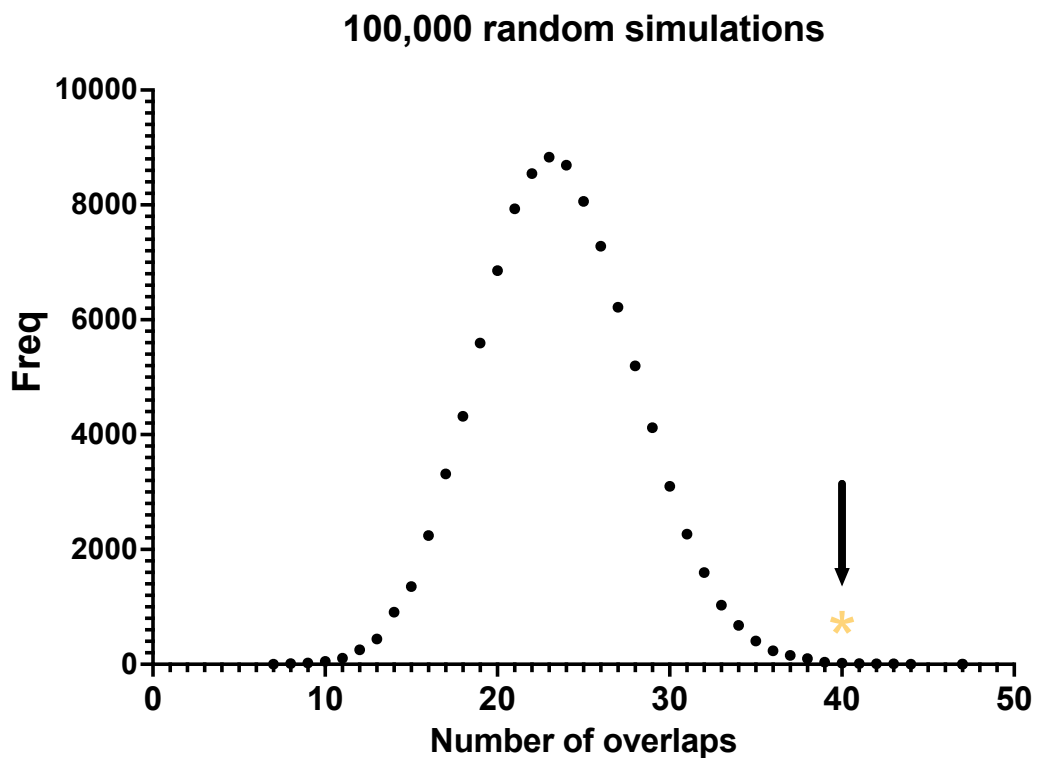
Supplementary figure 2: ~67% of interactions were retained, post- thresholding. Chart displays the percentage retention, 'post-threshold', compared with the pre-threshold interaction count ('Interactions') across the 9 interactomes. These counts have been obtained after interactions with 'UBC' have been excluded.

Supplementary figure 3



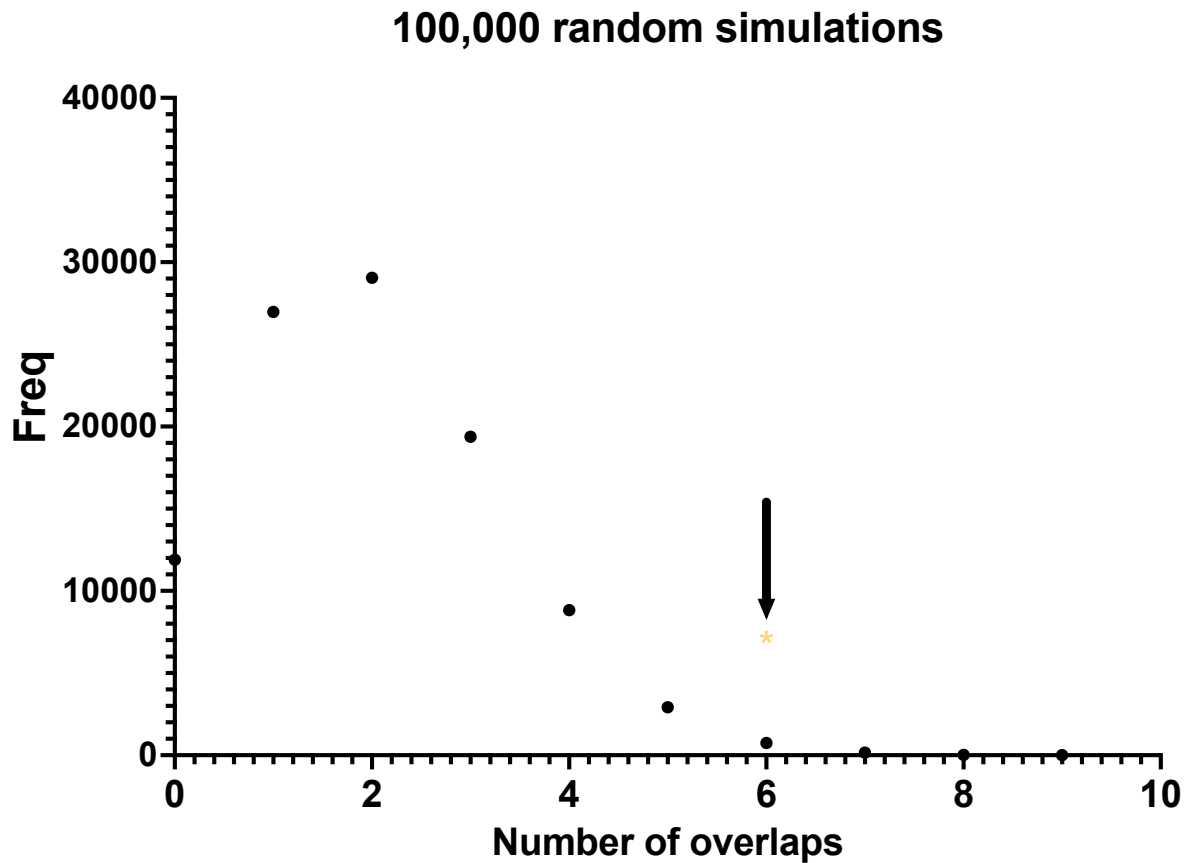
Supplementary figure 3: Proportion of interactions reaching the confidence score (CS) threshold (>2) captured by the PINOT (P), HIPPIE (H) and MIST (M) databases. There is significant overlap between the database searches, 86.9% of total interactions across the interactomes are captured by all 3. Of the 635 unique interactions; 90.9% are captured by PINOT, 93.8% by HIPPIE, with the highest proportion, 99%, captured by MIST.

Supplementary figure 4



Supplementary figure 4: Enrichment of PD associated genes in complete *Mito-CORE* network meets statistical significance. The normal distribution, generated by the **100,000 Random Simulations test for significance** reveals a mean of ~24 overlaps with 2638 random genes (number of unique interactors in the *Mito-CORE* network, excluding the NSL seeds). The true number of overlaps (40) is illustrated by a yellow star and arrow. The generated p -value for this significance =0.0002.

Supplementary figure 5



Supplementary figure 5: Enrichment of Mendelian PD genes in complete *Mito-CORE* network meets statistical significance. The normal distribution, generated by the **100,000 Random Simulations test for significance** reveals a mean of ~2 overlaps with 2638 random genes (number of unique interactors in the Mito-CORE network, excluding the NSL seeds). The true number of overlaps (6) is illustrated by a yellow star and arrow. The generated p -value for this significance = 0.001.